CLAIMS

1. A method of comparing one or more nucleic acid targets within two or more samples, comprising:

a) appending at least a first nucleic acid tag comprising a first amplification domain and a first differentiation domain to at least a first nucleic acid target of at least a first sample, wherein the first differentiation domain comprises a first primer binding domain, and wherein the differentiation domain of the first tag is appended between the first nucleic acid target sequence and the amplification domain;

b) appending at least a second nucleic acid tag comprising a second amplification domain and a second differentiation domain to at least the first nucleic acid target of at least a second sample, wherein the second differentiation domain comprises a second primer binding domain that is different than the first primer binding domain, and wherein the differentiation domain of the second tag is appended between the at least a first nucleic acid target sequence and the amplification domain;

c) co-amplifying the first nucleic acid target of the first sample and the first nucleic acid target of the second sample, wherein the amplifying produces at least a first amplified nucleic acid comprising at least the first primer binding domain and a segment of the target nucleic acid and a second amplified nucleic acid comprising at least the second primer binding domain and a segment of the target nucleic acid from the second sample;

d) differentiating the first amplified nucleic acid, wherein the differentiating comprises annealing at least a first differentiation primer to the first primer binding domain, wherein the differentiating further comprises extension of the first differentiation primer to produce at least a first differentiated nucleic acid;

e) differentiating the second amplified nucleic acid, wherein the differentiating further comprises annealing at least a second differentiation primer to the second primer binding domain, wherein the differentiating further comprises extension of the second differentiation primer to produce at least a second differentiated nucleic acid; and

f) comparing abundance of the differentiated nucleic acid from the first nucleic acid target of the first sample to abundance of the differentiated nucleic acid from the first nucleic acid target of the second sample.

2. The method of claim 1, wherein said first differentiated nucleic acid or the second differentiated nucleic acid includes a detectable moeity.

3. A method of comparing one or more single-stranded nucleic acid targets within two or more samples, comprising:

a) obtaining at least a first sample and a second sample, each potentially having at least a first nucleic acid target;

b) preparing at least a first tagged nucleic acid sample by appending at least a first nucleic acid tag comprising a first amplification domain and a first differentiation domain to the first nucleic acid target of the first sample, if the first nucleic acid target is present in the first sample;

c) preparing at least a second tagged nucleic acid sample by appending at least a second nucleic acid tag comprising a second amplification domain and a second differentiation domain to the first nucleic acid target of the second sample, if the first nucleic acid target is present in the second sample;

d) mixing the first tagged nucleic acid sample and the second tagged nucleic acid sample to create a sample mixture;

e) co-amplifying said first nucleic acid target of the first sample and said first nucleic acid target of the second sample in the sample mixture, if both the first and second nucelic acid targets are present in the sample mixture, wherein said co-amplifying produces at least a first amplified nucleic acid comprising at least the first differentiation domain and a segment of the target nucleic acid from the first sample, if the first nucleic acid target is present in the first sample, and at least a second amplified nucleic acid comprising at least the second differentiation domain and a segment of the target nucleic acid from the second sample, if the first nucleic acid target is present in the second sample;

f) differentiating the first amplified nucleic acid, if any, from the second amplified nucleic acid, if any; and

g) comparing abundance of the differentiated nucleic acid from the first nucleic acid target of said first sample to abundance of the differentiated nucleic acid from the first nucleic acid target of said second sample.

4. The method of claim 3, wherein the first nucleic acid target is present in the first sample.

5. The method of claim 4, wherein the first nucleic acid target is present in the second sample.

6. The method of claim 3, wherein the differentiation domain of the first tag and the second tag is appended between the first nucleic acid target sequence and the amplification domain.

7. The method of claim 3, wherein said nucleic acid target is one target of a plurality of nucleic acid targets within the samples.

8. The method of claim 3, wherein said first and second sample are two samples of a plurality of samples.

9. The method of claim 8, wherein the first and second tag are two tags of a plurality of tags.

10. The method of claim 3, wherein the amplification domain of the first nucleic acid tag and the second nucleic acid tag comprises a primer binding domain.

11. The method of claim 3, wherein the amplification domain of the first nucleic acid tag and the second nucleic acid tag comprises a transcription domain.

12. The method of claim 3, wherein the amplification domains of the first and second nucleic acid tags are functionally equivalent.

13. The method of claim 12, wherein the amplification domains of the first and second nucleic acid tags are identical.

14. The method of claim 3, wherein the differentiation domain of the first nucleic acid tag and the second nucleic acid tag comprise at least a primer binding domain, a transcription domain, a size differentiation domain, an affinity domain, a unique sequence domain, or a restriction enzyme domain.

15. The method of claim 3, wherein differentiating comprises production of at least one differentiated nucleic acid from said first or second amplified nucleic acid.

16. The method of claim 15, wherein said differentiated nucleic acid is labeled in a detectable manner.

17. The method of claim 3, wherein said differentiation domains of the first nucleic acid tag and the second nucleic acid tag are affinity domains.

18. The method of claim 17, wherein differentiating comprises binding at least a first ligand to at least a segment of the affinity domain.

19. The method of claim 18, wherein the first ligand comprises a nucleic acid.

20. The method of claim 18, wherein the first ligand is bound to a solid support.

21. The method of claim 20, wherein the first ligand is used to separate the first target nucleic acid from at least one other nucleic acid or molecule.

22. The method of claim 20, wherein the solid support is a membrane, a bead, a glass slide, or a microtiter well.

23. The method of claim 20, wherein the amplified nucleic acid is labeled in a detectable manner.

24. The method of claim 18, wherein the first ligand is labeled.

25. The method of claim 24, wherein binding of the first ligand to said segment of the affinity domain results in a detectable signal.

26. The method of claim 3, wherein said differentiation domain of the first nucleic acid tag and the differentiation domain of the second nucleic acid tag are primer binding domains.

27. The method of claim 26, wherein differentiating comprises binding at least a first differentiation primer to at least one segment of the primer binding domain.

28. The method of claim 27, further comprising at least one primer extension reaction.

29. The method of claim 28, wherein said primer extension reaction produces at least one differentiated nucleic acid.

30. The method of claim 29, wherein said differentiated nucleic acid is labeled with a detectable moiety.

31. The method of claim 3, wherein said differentiation domains of the first and second nucleic acids are unique sequence domains.

32. The method of claim 31, wherein differentiating comprises sequencing through the differentiation domains of the amplified nucleic acids.

33. The method of claim 3, wherein the differentiation domains of the first nucleic acid tag and the second nucleic acid tag each comprise at least one transcription domain.

34. The method of claim 33, wherein said differentiation domain comprises a promoter for a prokaryotic RNA polymerase.

35. The method of claim 33, wherein differentiating comprises a transcription reaction.

36. The method of claim 35, wherein said transcription reaction produces at least one differentiated nucleic acid.

37. The method of claim 36, wherein said differentiated nucleic acid includes a detectable moiety.

38. The method of claim 3, wherein the differentiation domain of the first nucleic acid tag and the second nucleic acid tag each comprise at least one size differentiation domain.

39. The method of claim 38, wherein said differentiating comprises distinguishing the amplification products from the first and second samples by size.

40. The method of claim 3, wherein said differentiation domain of the first nucleic acid tag or the second nucleic acid tag comprises at least one restriction enzyme cleavage domain.

41. The method of claim 40, further comprising cleaving said restriction enzyme cleavage site to promote the ligation of a label or at least one additional domain to a segment of the at least a first or at least a second nucleic acid tag.

42. The method of claim 40, wherein differentiating comprises cleaving said restriction enzyme site to remove at least one label.

43. The method of claim 3, wherein the first nucleic acid tag or the second nucleic acid tag further comprises at least one additional domain.

44. The method of claim 43, wherein said additional domain is labeling domain, a restriction enzyme domain, a secondary amplification domain, a secondary differentiation domain or a sequencing primer binding domain.

45. The method of claim 43, wherein said additional domain comprises at least one labeling domain.

46. The method of claim 45, wherein said labeling domain is comprised between the differentiation domain and the amplification domain.

47. A method of comparing one or more nucleic acid targets within two or more samples, comprising:

a) appending at least a first nucleic acid tag comprising at least a first amplification domain and at least a first differentiation domain to at least a first nucleic acid target of at least a first sample, wherein said first differentiation domain comprises at least one affinity domain, primer binding domain, or transcription domain;

b) appending at least a second nucleic acid tag comprising at least a second amplification domain and at least a second differentiation domain to the first nucleic acid target of at least a second sample, wherein the second

differentiation domain is different than the first differentiation domain and comprises at least one affinity domain, primer binding domain, or transcription domain;

c) co-amplifying said first nucleic acid target of the first sample and said first nucleic acid target of the second sample, wherein said amplifying produces at least a first amplified nucleic acid comprising at least the first differentiation domain and a segment of the target nucleic acid from the first sample and at least a second amplified nucleic acid comprising at least the second differentiation domain and a segment of the target nucleic acid from the second sample;

d) differentiating the first amplified nucleic acid from the second amplified nucleic acid; and

e) comparing abundance of the differentiated nucleic acid from the first nucleic acid target of said first sample to abundance of the differentiated nucleic acid from the first nucleic acid target of said second sample.

48. A method of comparing one or more nucleic acid targets within two or more samples, comprising:

a) appending at least a first nucleic acid tag comprising a first amplification domain and a first differentiation domain to at least a first nucleic acid target of at least a first sample, wherein the first differentiation domain comprises a first transcription domain, and wherein the differentiation domain of the first tag is appended between the first nucleic acid target sequence and the amplification domain;

b) appending at least a second nucleic acid tag comprising a second amplification domain and a second differentiation domain to the first nucleic acid target of at least a second sample, wherein the second differentiation domain comprises

a second transcription domain that is different than the first transcription domain, and wherein the differentiation domain of the second tag is appended between the at least a first nucleic acid target sequence and the amplification domain;

c) co-amplifying the first nucleic acid target of the first sample and the first nucleic acid target of the second sample, wherein the amplifying produces at least a first amplified nucleic acid comprising the at least first transcription domain and a segment of the target nucleic acid from the first sample and a second amplified nucleic acid comprising at least the second transcription domain and a segment of the target nucleic acid from the second sample;

d) differentiating the first amplified nucleic acid, wherein the differentiating comprises transcription from the first transcription domain to produce at least a first differentiated nucleic acid;

e) differentiating the second amplified nucleic acid, wherein the differentiating further comprises transcription from the second transcription domain to produce at least a second differentiated nucleic acid; and

f) comparing abundance of the differentiated nucleic acid from the first nucleic acid target of said first sample to abundance of the differentiated nucleic acid from the first nucleic acid target of said second sample.

49. The method of claim 48, wherein each of the first and second differentiated nucleic acids comprise at least one detectable moeity.

50. A method of comparing one or more single-stranded nucleic acid targets within two or more samples, comprising:

a) appending at least a first single-stranded nucleic acid tag comprising a first amplification domain and a first differentiation domain to at least a first

nucleic acid target of at least a first sample, wherein the first differentiation domain comprises a first size differentiation domain, and wherein the differentiation domain of the first tag is appended between the first nucleic acid target sequence and the amplification domain;

b) appending at least a second single-stranded nucleic acid tag comprising a second amplification domain and a second differentiation domain to the first nucleic acid target of at least a second sample, wherein the second differentiation domain comprises a second size differentiation domain that is different than the first size differentiation domain, and wherein the differentiation domain of the second tag is appended between the at least a first nucleic acid target sequence and the amplification domain;

c) co-amplifying the first nucleic acid target of the first sample and the first nucleic acid target of the second sample, wherein the co-amplifying produces at least a first amplified nucleic acid comprising at least the first size differentiation domain and a segment of the target nucleic acid and a second amplified nucleic acid comprising at least the second size differentiation domain and a segment of the target nucleic acid;

d) differentiating the first amplified nucleic acid, wherein said differentiating comprises determining the electrophoretic mobility of the first amplified nucleic acid;

e) differentiating the second amplified nucleic acid, wherein said differentiating further comprises determining the electrophoretic mobility of the second amplified nucleic acid; and

f) comparing abundance of the differentiated nucleic acid from the first nucleic acid target of said first sample to abundance of the differentiated nucleic acid from the first nucleic acid target of said second sample.

51. A method of comparing one or more nucleic acid targets within two or more samples, comprising:

a) appending at least a first nucleic acid tag comprising a first amplification domain and a first differentiation domain to at least a first nucleic acid target of at least a first sample, wherein the first differentiation domain comprises a first affinity domain, and wherein the differentiation domain of the first tag is appended between the first nucleic acid target sequence and the amplification domain;

b) appending at least a second nucleic acid tag comprising a second amplification domain and a second differentiation domain to the first nucleic acid target of at least a second sample, wherein the second differentiation domain comprises a second affinity domain that is different than the first affinity domain, and wherein the differentiation domain of the second tag is appended between the at least a first nucleic acid target sequence and the amplification domain;

c) co-amplifying the first nucleic acid target of the first sample and the first nucleic acid target of the second sample to produce at least a first amplified nucleic acid comprising at least the first affinity domain and a segment of the target nucleic acid from the first sample and a second amplified nucleic acid comprising at least the second affinity domain and a segment of the target nucleic acid from the second sample;

d) differentiating the first amplified nucleic acid, wherein the differentiating comprises binding of the first amplified nucleic acid to an at least a first ligand;

f) differentiating the second amplified nucleic acid, wherein the differentiating further comprises binding of the second amplified nucleic acid to an at least a second ligand; and

g) comparing abundance of the differentiated nucleic acid from the first nucleic acid target of said first sample to abundance of the differentiated nucleic acid from the first nucleic acid target of said second sample.

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